

45  
-1/102

SEQUENCE LISTING

<110> Dattwyler, Raymond J.  
Seinost, Gerald  
Dykhuisen, Daniel  
Luft, Benjamin J.  
Maria J.C. Gomes-Solecki

<120> Groups of *Borrelia burgdorferi* and  
*Borrelia afzelii* That Cause Lyme Disease in Humans

<130> 2631.1002-001

<150> US 60/140,042  
<151> 1999-06-18

<160> 84

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35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
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165 170 175

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50 55 60  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
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85 90 95  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
100 105 110  
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115 120 125  
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Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
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35 40 45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288  
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
85 90 95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336  
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432  
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130 135 140

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
145 150 155 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528  
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
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35 40 45  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80  
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85 90 95

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Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125  
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
130 135 140  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
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aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30  
aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144  
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala  
35 40 45  
gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att gct gct 192  
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala  
50 55 60  
aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat acc gaa 240  
Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu  
65 70 75 80  
aat aat cac aat gga tca ttg tta gcg gga gct tat gca ata tca acc 288  
Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr  
85 90 95  
cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta aag gaa 336  
Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu  
100 105 110  
aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat aaa tta 384  
Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu  
115 120 125  
aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat gct gat 432  
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130 135 140

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145 150 155 160  
gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca aaa gca 528  
Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala  
165 170 175  
gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct gtt 576  
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Val

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35 40 45  
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala  
50 55 60  
Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu  
65 70 75 80  
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85 90 95  
Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu  
100 105 110  
Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu  
115 120 125  
Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp  
130 135 140  
Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala  
145 150 155 160  
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180 185 190  
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aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt	96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu	
20 25 30	
aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct	144
Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala	
35 40 45	
gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt gct aaa	192
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys	
50 55 60	
gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat gaa gca	240
Ala Ile Gly Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala	
65 70 75 80	
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Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu	
85 90 95	
ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta aag gaa	336
Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu	
100 105 110	
aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act aaa cta	384
Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu	
115 120 125	
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Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn	
130 135 140	
gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat aag ggc	480
Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Gly Lys Asp Lys Gly	
145 150 155 160	
gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta tca aaa	528
Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys	
165 170 175	
gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct	576
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Val Val	

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<213> Borrelia brgdorferi

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35 40 45  
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys  
50 55 60  
Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala  
65 70 75 80  
Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu  
85 90 95  
Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu  
100 105 110  
Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu  
115 120 125  
Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn  
130 135 140  
Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly  
145 150 155 160  
Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys  
165 170 175  
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180 185 190  
Val Val

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1 5 10 15  
aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
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aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144  
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45  
gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192  
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60

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agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta	288
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu	
85 90 95	
ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag	336
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys	
100 105 110	
att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa	384
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys	
115 120 125	
agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca	432
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala	
130 135 140	
caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca	480
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala	
145 150 155 160	
gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct	528
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala	
165 170 175	
caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg	576
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val	
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35 40 45  
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60  
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln  
65 70 75 80  
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu  
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115 120 125  
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala  
130 135 140

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Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala  
145 150 155 160  
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala  
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Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val  
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aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt 96  
Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30  
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144  
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35 40 45  
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Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
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aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag 240  
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln  
65 70 75 80  
agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta 288  
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu  
85 90 95  
ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag 336  
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Leu Lys Glu Lys  
100 105 110  
att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa 384  
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys  
115 120 125  
agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca 432  
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala  
130 135 140  
caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca 480  
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala  
145 150 155 160

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11/102

gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528  
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala  
165 170 175

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576  
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val  
180 185 190

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35 40 45  
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60  
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln  
65 70 75 80  
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu  
85 90 95  
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys  
100 105 110  
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys  
115 120 125  
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala  
130 135 140  
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala  
145 150 155 160  
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165 170 175  
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val  
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Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly  
1 5 10 15

aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30

56  
12/102

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc	144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala	
35 40 45	
gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa	192
Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys	
50 55 60	
gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca	240
Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala	
65 70 75 80	
gat cac aac gga tca tta ata tca gga gca tat tta att tca aac tta	288
Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu	
85 90 95	
ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca	336
Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala	
100 105 110	
gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta	384
Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu	
115 120 125	
aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat	432
Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn	
130 135 140	
gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc gct	480
Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala	
145 150 155 160	
gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca	528
Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala	
165 170 175	
gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc cct	573
Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro	
180 185 190	

<210> 18  
<211> 191  
<212> PRT  
<213> Borrelia burgdorferi

<400> 18  
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly  
1 5 10 15  
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30  
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45  
Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys  
50 55 60  
Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala  
65 70 75 80

AI  
com. +

57  
43/102

Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu  
85 90 95  
Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala  
100 105 110  
Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu  
115 120 125  
Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn  
130 135 140  
Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala  
145 150 155 160  
Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala  
165 170 175  
Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro  
180 185 190

*AI, x*  
*cm*  
<210> 19  
<211> 553  
<212> DNA  
<213> *Borrelia burgdorferi*

<220>  
<221> CDS  
<222> (1)...(553)

<400> 19  
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Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly  
1 5 10 15  
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30  
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct 144  
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45  
gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act 192  
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60  
aaa gct att ggt aaa aaa ata gat aac aat gct ggt ttg ggt gct gaa 240  
Lys Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu  
65 70 75 80  
gtg ggt caa aac gga tca ttg cta gca gga gct tat gca atc tca act 288  
Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr  
85 90 95  
gta ata ata gaa aaa ttg agc aca tta aaa aat gta gaa gaa tta aaa 336  
Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys  
100 105 110  
gaa aaa att aca aag gct aag gat tgt tct gaa aaa ttc act aaa aaa 384  
Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys  
115 120 125

58  
44/102

tta aaa gat agc cgc gca gag ctt ggt aaa aaa gat gcc agt gat gat	432
Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp	
130 135 140	
gat gca aaa aaa gct att tta aaa aca aat caa gct aac gat aag ggt	480
Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly	
145 150 155 160	
gct aaa gaa ctt aaa gag tta ttt gaa gca gta gaa agc ttg tca aaa	528
Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys	
165 170 175	
gcg gct aaa gag atg cta aac aag t	553
Ala Ala Lys Glu Met Leu Asn Lys	
180	

AI  
com. +

<210> 20  
<211> 184  
<212> PRT  
<213> Borrelia burgdorferi

<400> 20  
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly  
1 5 10 15  
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30  
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45  
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60  
Lys Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu  
65 70 75 80  
Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr  
85 90 95  
Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Leu Lys  
100 105 110  
Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys  
115 120 125  
Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp  
130 135 140  
Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly  
145 150 155 160  
Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys  
165 170 175  
Ala Ala Lys Glu Met Leu Asn Lys  
180

<210> 21  
<211> 582  
<212> DNA  
<213> Borrelia burgdorferi

<220>  
<221> CDS  
<222> (1) ... (582)

<400> 21

59  
15/102

atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg 48  
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly  
1 5 10 15

aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
20 25 30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct 144  
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45

gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act 192  
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60

aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa 240  
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu  
65 70 75 80

gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca aaa 288  
Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys  
85 90 95

cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag 336  
Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys  
100 105 110

gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa 384  
Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys  
115 120 125

cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat gag 432  
Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu  
130 135 140

aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag ggc 480  
Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly  
145 150 155 160

gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa 528  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys  
165 170 175

gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agt cct 576  
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro  
180 185 190

att gtg 582  
Ile Val

<210> 22  
<211> 194  
<212> PRT  
<213> *Borrelia burgdorferi*

<400> 22

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167102

Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly  
1 5 10 15  
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20 25 30  
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
35 40 45  
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
50 55 60  
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu  
65 70 75 80  
Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys  
85 90 95  
Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys  
100 105 110  
Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys  
115 120 125  
Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu  
130 135 140  
Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly  
145 150 155 160  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys  
165 170 175  
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro  
180 185 190  
Ile Val

AI  
con't

<210> 23  
<211> 1128  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1128)

<400> 23 48  
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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60

61  
~~177/102~~

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
65 70 75 80  
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Thr Asn Gly Thr Lys Thr Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala  
180 185 190  
atg gta aat aat tca ggg aaa gat ggg aat aca tct gca aat tct gct 624  
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
195 200 205  
gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672  
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile  
210 215 220  
aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg 720  
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu  
225 230 235 240  
ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata aaa 768  
Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys  
245 250 255  
aac gat gtt agt tta gat aat gag gca gat cac aac gga tca tta ata 816  
Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile  
260 265 270  
tca gga gca tat tta att tca aac tta ata aca aaa aaa ata agt gca 864  
Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala  
275 280 285  
ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct aag aaa 912  
Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys  
290 295 300

A1  
cont

62  
107102

tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca gat ctt 960  
Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu  
305 310 315 320

ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att tta aaa 1008  
Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys  
325 330 335

aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag tta ttt 1056  
Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe  
340 345 350

gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt act aat 1104  
Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn  
355 360 365

tca gtt aaa gag ctt aca agc taa 1128  
Ser Val Lys Glu Leu Thr Ser \*  
370 375

A)  
Cm, X

<210> 24  
<211> 375  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

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1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 30  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 45  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys 60  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser 80  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 95  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 110  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 125  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 140  
130 135 140  
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 160  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 175  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala 190  
180 185 190  
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala 205  
195 200 205  
Asp Glu Ser Val Lys Glu Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile 220  
210 215 220

63  
197102

Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu  
225 230 235 240  
Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys  
245 250 255  
Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile  
260 265 270  
Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala  
275 280 285  
Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys  
290 295 300  
Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu  
305 310 315 320  
Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys  
325 330 335  
Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe  
340 345 350  
Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn  
355 360 365  
Ser Val Lys Glu Leu Thr Ser  
370 375

A1  
Cm X  
<210> 25  
<211> 1124  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1124)

<400> 25  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15 48

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30 96

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45 144

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60 192

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
65 70 75 80 240

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95 288

64  
207102

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala  
180 185 190

atg gta aat aat tca gga aaa gat ggg aat aca tct gca aat tct gct 624  
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
195 200 205

gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672  
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile  
210 215 220

aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg 720  
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu  
225 230 235 240

ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa aaa ata 768  
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Ile  
245 250 255

caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg 816  
Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu  
260 265 270

tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa tta gat 864  
Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp  
275 280 285

gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat gct aag 912  
Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys  
290 295 300

aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat gcg caa 960  
Lys Cys Ser Glu Asp Phe Thr Lys Leu Glu Gly Glu His Ala Gln  
305 310 315 320

ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct att tta 1008  
Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
325 330 335

A1  
cm

65  
-21/102

ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa aag cta 1056  
Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu  
340 345 350

ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg ctt gct 1104  
Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala  
355 360 365

aat tca gtt aaa gag ctt ac 1124  
Asn Ser Val Lys Glu Leu  
370

A  
cm.t  
<210> 26  
<211> 374  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 26  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala  
180 185 190  
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
195 200 205  
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile  
210 215 220  
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu  
225 230 235 240  
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile  
245 250 255  
Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu  
260 265 270  
Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp  
275 280 285

66  
227102

Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys  
290 295 300  
Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln  
305 310 315 320  
Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
325 330 335  
Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu  
340 345 350  
Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala  
355 360 365  
Asn Ser Val Lys Glu Leu  
370

*AI X*  
<210> 27  
<211> 1137  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1) ... (1137)

<400> 27  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125

*67*  
23/102

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 576  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
180 185 190

aaa cct tcc atg gta aat aat tca ggg aaa gat ggg aat aca tct gca 624  
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala  
195 200 205

aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt 672  
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
210 215 220

aaa aaa att aca gaa tct aac gca gtt ctc gcc gtg aaa gaa gtt 720  
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val  
225 230 235 240

gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa 768  
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys  
245 250 255

aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga 816  
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly  
260 265 270

tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa 864  
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys  
275 280 285

ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag 912  
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys  
290 295 300

gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac 960  
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His  
305 310 315 320

aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc 1008  
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala  
325 330 335

att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa 1056  
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu  
340 345 350

aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg 1104  
Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met  
355 360 365

*AI  
cm. x*

ctt act aat tca gtt aaa gag ctt aca agc taa  
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser \*  
370 375

<210> 28  
<211> 378  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

A1 X  
Cm

<400> 28  
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
180 185 190  
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala  
195 200 205  
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
210 215 220  
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val  
225 230 235 240  
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys  
245 250 255  
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly  
260 265 270  
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys  
275 280 285  
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys  
290 295 300  
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His  
305 310 315 320  
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala  
325 330 335  
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu  
340 345 350

69  
25/102

Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met  
355 360 365  
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
370 375

<210> 29  
<211> 1133  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1133)

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cmx*  
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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160

70  
26/102

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 576  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
180 185 190

aaa cct tcc atg gta aat aat tca gga aaa gat ggg aat aca tct gca 624  
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala  
195 200 205

aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt 672  
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
210 215 220

aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att 720  
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile  
225 230 235 240

gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt 768  
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly  
245 250 255

aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat 816  
Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn  
260 265 270

gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa 864  
Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln  
275 280 285

aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa 912  
Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu  
290 295 300

aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa 960  
Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu  
305 310 315 320

cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa 1008  
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys  
325 330 335

gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt 1056  
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu  
340 345 350

gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag 1104  
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu  
355 360 365

atg ctt gct aat tca gtt aaa gag ctt ac 1133  
Met Leu Ala Asn Ser Val Lys Glu Leu  
370 375

<210> 30  
<211> 377

71  
27/102

<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 30  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
Lys Ala Asn Gly Thr Lys Thr Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
180 185 190  
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala  
195 200 205  
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
210 215 220  
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile  
225 230 235 240  
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly  
245 250 255  
Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn  
260 265 270  
Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln  
275 280 285  
Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu  
290 295 300  
Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu  
305 310 315 320  
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys  
325 330 335  
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu  
340 345 350  
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu  
355 360 365  
Met Leu Ala Asn Ser Val Lys Glu Leu  
370 375

<210> 31  
<211> 1112

72  
28/102

<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1) ... (1112)

<400> 31

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
100 105 110

aaa tgc tct gaa gag ttt agt act act aaa cta aaa gat aat cat gca cag 384  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190

AI  
Cm

73  
-29/102

tca aga aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt 624  
Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val  
195 200 205

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac 672  
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
210 215 220

gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata 720  
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile  
225 230 235 240

gat gaa ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt 768  
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly  
245 250 255

tta gag gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat 816  
Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr  
260 265 270

gca ata tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa 864  
Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu  
275 280 285

gaa tta aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt 912  
Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe  
290 295 300

act aat aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt 960  
Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu  
305 310 315 320

act gat gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa 1008  
Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys  
325 330 335

gat aag ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac 1056  
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn  
340 345 350

tta tca aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt 1104  
Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu  
355 360 365

aca agt cc 1112  
Thr Ser  
370

<210> 32  
<211> 370  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 32

AI  
cm't

74  
30/102

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190  
Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val  
195 200 205  
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
210 215 220  
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile  
225 230 235 240  
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly  
245 250 255  
Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr  
260 265 270  
Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu  
275 280 285  
Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe  
290 295 300  
Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu  
305 310 315 320  
Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys  
325 330 335  
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn  
340 345 350  
Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu  
355 360 365  
Thr Ser  
370

<210> 33  
<211> 1113  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

75  
~~31/102~~

<221> CDS  
<222> (1) ... (1113)

<400> 33

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190

tca ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt 624  
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val  
195 200 205

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac 672  
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
210 215 220

A  
cm X

76  
-327102

gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata 720  
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile  
225 230 235 240

gat gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt 768  
Asp Glu Leu Ala Lys Ala Ile Gly Lys Ile Lys Asn Asp Val Ser  
245 250 255

tta gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat 816  
Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr  
260 265 270

tta att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca 864  
Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser  
275 280 285

gga gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa 912  
Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu  
290 295 300

ttt act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc 960  
Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly  
305 310 315 320

gtt act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat 1008  
Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp  
325 330 335

aaa act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa 1056  
Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys  
340 345 350

aac ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag 1104  
Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu  
355 360 365

ctt aca agc 1113  
Leu Thr Ser  
370

<210> 34  
<211> 371  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 34  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60

AI  
CM

Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190  
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val  
195 200 205  
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
210 215 220  
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile  
225 230 235 240  
Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser  
245 250 255  
Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr  
260 265 270  
Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser  
275 280 285  
Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu  
290 295 300  
Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly  
305 310 315 320  
Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp  
325 330 335  
Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys  
340 345 350  
Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu  
355 360 365  
Leu Thr Ser  
370

<210> 35  
<211> 1112  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1) ... (1112)

<400> 35  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

78  
347102

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190

tca gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt 624  
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val  
195 200 205

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac 672  
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
210 215 220

gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata 720  
Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile  
225 230 235 240

gat gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt 768  
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly  
245 250 255

A1  
cm

79  
357102

ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct 816  
Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala  
260 265 270

tat aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat 864  
Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn  
275 280 285

tca gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa 912  
Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu  
290 295 300

gat ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa 960  
Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu  
305 310 315 320

aat gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca 1008  
Asn Val Thr Asp Glu Asn Ala Lys Ala Ile Leu Ile Thr Asp Ala  
325 330 335

gct aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta 1056  
Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val  
340 345 350

gaa aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa 1104  
Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys  
355 360 365

gag ctt ac 1112  
Glu Leu  
370

<210> 36  
<211> 370  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 36  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

AI  
Cm.t

80  
36/102

Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190  
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val  
195 200 205  
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
210 215 220  
Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile  
225 230 235 240  
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly  
245 250 255  
Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala  
260 265 270  
Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn  
275 280 285  
Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu  
290 295 300  
Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu  
305 310 315 320  
Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala  
325 330 335  
Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val  
340 345 350  
Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys  
355 360 365  
Glu Leu  
370

AI  
cm X  
<210> 37  
<211> 1106  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1106)

<400> 37  
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144  
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45

81  
377102

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288  
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
85 90 95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336  
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432  
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
130 135 140

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
145 150 155 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528  
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
165 170 175

gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca aga 576  
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg  
180 185 190

aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg 624  
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly  
195 200 205

cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt 672  
Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val  
210 215 220

gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa 720  
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu  
225 230 235 240

ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag 768  
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu  
245 250 255

gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata 816  
Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile  
260 265 270

tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta 864  
Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu  
275 280 285

AI  
cm.t

82  
38/102

aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat 912  
Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn  
290 295 300

aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat 960  
Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp  
305 310 315 320

gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag 1008  
Asp Asn Ala Gln Arg Ala Ile Leu Lys His Ala Asn Lys Asp Lys  
325 330 335

ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca 1056  
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser  
340 345 350

aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt 1104  
Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser  
355 360 365

cc 1106

A1  
Cm

<210> 38  
<211> 368  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 38  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80  
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
85 90 95  
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125  
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
130 135 140  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
145 150 155 160  
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
165 170 175  
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg  
180 185 190  
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly  
195 200 205

83  
39/102

Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val  
210 215 220  
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu  
225 230 235 240  
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu  
245 250 255  
Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile  
260 265 270  
Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu  
275 280 285  
Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn  
290 295 300  
Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp  
305 310 315 320  
Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys  
325 330 335  
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser  
340 345 350  
Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser  
355 360 365

A1  
cm.†

<210> 39  
<211> 1107  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1107)

<400> 39  
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144  
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288  
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
85 90 95

84  
40/102

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336  
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432  
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
130 135 140

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
145 150 155 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528  
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
165 170 175

AI +  
cmt

gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca ggg 576  
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly  
180 185 190

aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg 624  
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly  
195 200 205

cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt 672  
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val  
210 215 220

gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag 720  
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu  
225 230 235 240

ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat 768  
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp  
245 250 255

aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta att 816  
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile  
260 265 270

tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa 864  
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu  
275 280 285

ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act 912  
Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr  
290 295 300

gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act 960  
Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr  
305 310 315 320

gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act 1008  
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr  
325 330 335

aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg 1056  
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu  
 340 345 350

tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca 1104  
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr  
 355 360 365

1107

agc  
 Ser

<210> 40  
 <211> 369  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<400> 40  
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
 1 5 10 15  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30  
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
 35 40 45  
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
 50 55 60  
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
 65 70 75 80  
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
 85 90 95  
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
 100 105 110  
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
 115 120 125  
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
 130 135 140  
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
 145 150 155 160  
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
 165 170 175  
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly  
 180 185 190  
 Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly  
 195 200 205  
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val  
 210 215 220  
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu  
 225 230 235 240  
 Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp  
 245 250 255  
 Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile  
 260 265 270  
 Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu  
 275 280 285

A1  
 Cm't

86  
427102

Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr  
290 295 300  
Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr  
305 310 315 320  
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr  
325 330 335  
Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu  
340 345 350  
Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr  
355 360 365  
Ser

*AI*  
*Chimera*  
<210> 41  
<211> 1106  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<221> CDS  
<222> (1)...(1106)

<400> 41 48  
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144  
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288  
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
85 90 95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336  
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125

87  
43/102

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432  
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
130 135 140

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
145 150 155 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528  
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
165 170 175

gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca gga 576  
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly  
180 185 190

aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg 624  
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly  
195 200 205

cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt 672  
Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val  
210 215 220

gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa 720  
Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu  
225 230 235 240

ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta 768  
Leu Ala Thr Lys Ala Ile Gly Lys Ile Gln Gln Asn Gly Gly Leu  
245 250 255

gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca 816  
Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr  
260 265 270

ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa 864  
Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu  
275 280 285

aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt 912  
Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe  
290 295 300

act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt 960  
Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val  
305 310 315 320

act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa 1008  
Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys  
325 330 335

gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac 1056  
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn  
340 345 350

ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt 1104  
Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
355 360 365

A1  
Cn.t

ac

<210> 42  
<211> 368  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> OspC Chimera

<400> 42  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45  
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
65 70 75 80  
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
85 90 95  
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
100 105 110  
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
115 120 125  
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
130 135 140  
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
145 150 155 160  
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
165 170 175  
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly  
180 185 190  
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly  
195 200 205  
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val  
210 215 220  
Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu  
225 230 235 240  
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu  
245 250 255  
Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr  
260 265 270  
Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu  
275 280 285  
Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe  
290 295 300  
Thr Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val  
305 310 315 320  
Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys  
325 330 335  
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn  
340 345 350  
Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
355 360 365

AI  
cm.t

89  
457102

<210> 43  
<211> 633  
<212> DNA  
<213> *Borrelia burgdorferi*

<220>  
<221> CDS  
<222> (1)...(633)

<400> 43 48  
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
5 10 15  
1 5 10 15  
ata tct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 96  
Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
20 25 30  
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 144  
Al Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
35 40 45  
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 192  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
50 55 60  
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 240  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
65 70 75 80  
ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 288  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
85 90 95  
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 336  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
100 105 110  
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 384  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
115 120 125  
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 432  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
130 135 140  
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 480  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
145 150 155 160  
aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 528  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
165 170 175  
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 576  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
180 185 190

AI  
Com. +

90  
~~461102~~

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 624  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
195 200 205

624

aaa cct taa  
Lys Pro \*  
210

633

<210> 44  
<211> 210  
<212> PRT  
<213> Borrelia burgdorferi

<400> 44  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15  
Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
20 25 30  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
35 40 45  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
50 55 60  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
65 70 75 80  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
85 90 95  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
100 105 110  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
115 120 125  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
130 135 140  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
145 150 155 160  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
165 170 175  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
180 185 190  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
195 200 205

Lys Pro  
210

<210> 45  
<211> 580  
<212> DNA  
<213> Borrelia burgdorferi

<220>  
<221> CDS  
<222> (1) ... (580)

<400> 45  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

91  
477102

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Ala Asn Gly Thr Lys Thr Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca tcc 576  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser  
180 185 190

atg g 580  
Met

<210> 46  
<211> 193  
<212> PRT  
<213> *Borrelia burgdorferi*

<400> 46  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30

92  
48/102

Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser  
180 185 190  
Met

A1  
cm.t

<210> 47  
<211> 639  
<212> DNA  
<213> Borrelia garinii

<220>  
<221> CDS  
<222> (1)...(639)

<400> 47 48  
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15

ata tct tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat 96  
Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn  
20 25 30

cct gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa 144  
Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
35 40 45

aaa att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag 192  
Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu  
50 55 60

act ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa 240  
Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln  
65 70 75 80

aaa ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga 288  
Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly  
85 90 95

93  
497102

tcg ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa . 336  
Ser Leu Leu Ala Gly Ala Tyr Ala Ser Thr Leu Ile Thr Glu Lys  
100 105 110

ttg agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag . 384  
Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys  
115 120 125

gct aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat . 432  
Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His  
130 135 140

gca gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct . 480  
Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala  
145 150 155 160

att tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa . 528  
Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys  
165 170 175

gat tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca . 576  
Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala  
180 185 190

cta act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt . 624  
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser  
195 200 205

cca aaa aaa cct taa . 639  
Pro Lys Lys Pro \*  
210

<210> 48  
<211> 212  
<212> PRT  
<213> Borrelia garinii

<400> 48  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15  
Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn  
20 25 30  
Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
35 40 45  
Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu  
50 55 60  
Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln  
65 70 75 80  
Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly  
85 90 95  
Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys  
100 105 110  
Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys  
115 120 125  
Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His  
130 135 140  
Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala  
145 150 155 160

AI  
cm.t

94  
50/102

Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys  
165 170 175  
Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala  
180 185 190  
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser  
195 200 205  
Pro Lys Lys Pro  
210

*AI*  
*Cm. X*  
<210> 49  
<211> 624  
<212> DNA  
<213> Borrelia afzelii

<220>  
<221> CDS  
<222> (1)...(624)

<400> 49  
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15

ata tct tgt aat aat tca ggt ggg gat tct gca tct act aat cct gat 96  
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp  
20 25 30

gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa att aca 144  
Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr  
35 40 45

gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt 192  
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu  
50 55 60

tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat 240  
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn  
65 70 75 80

gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg ata gca 288  
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala  
85 90 95

gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt gta ttg 336  
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu  
100 105 110

aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat tgt tcc 384  
Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser  
115 120 125

caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt ggt ata 432  
Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile  
130 135 140

caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa aca cat 480  
Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His  
145 150 155 160

95  
51/102

gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca 528  
Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser  
165 170 175  
cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat tca gtt 576  
Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val  
180 185 190  
aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 624  
Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro \*  
195 200 205

A1  
cm, t

<210> 50  
<211> 207  
<212> PRT  
<213> Borrelia afzelii

<400> 50  
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
1 5 10 15  
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp  
20 25 30  
Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr  
35 40 45  
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu  
50 55 60  
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn  
65 70 75 80  
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala  
85 90 95  
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu  
100 105 110  
Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser  
115 120 125  
Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile  
130 135 140  
Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His  
145 150 155 160  
Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser  
165 170 175  
Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val  
180 185 190  
Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
195 200 205

<210> 51  
<211> 1680  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1680)

<400> 51

96  
527102

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Thr Asn Gly Thr Lys Thr Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala  
180 185 190

atg ggt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct 624  
Met Gly Ser Asn Ser Gly Lys Gly Asp Ser Ala Ser Thr Asn Pro  
195 200 205

gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa 672  
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
210 215 220

att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act 720  
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr  
225 230 240

A  
C  
X

97  
53/102

ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa 768  
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys  
245 250 255

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 816  
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
260 265 270

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg 864  
Leu Leu Ala Gly Ala Tyr Ala Ser Thr Leu Ile Thr Glu Lys Leu  
275 280 285

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct 912  
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala  
290 295 300

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca 960  
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala  
305 310 315 320

al t  
cm

gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att 1008  
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile  
325 330 335

tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat 1056  
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
340 345 350

tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta 1104  
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
355 360 365

act aat tca gtt aaa gaa ctt ggt cac cgt aat aat tca ggt ggg gat 1152  
Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp  
370 375 380

tct gca tct act aat cct gat gag tct gca aaa gga cct aat ctt acc 1200  
Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr  
385 390 395 400

gta ata agc aaa aaa att aca gat tct aat gca ttt tta ctg gct gtg 1248  
Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val  
405 410 415

aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt tct aaa gct 1296  
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala  
420 425 430

att ggt aaa aaa ata aaa aat gat ggt act tta gat aac gaa gca aat 1344  
Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn  
435 440 445

cga aac gaa tca ttg ata gca gga gct tat gaa ata tca aaa cta ata 1392  
Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile  
450 455 460

98  
54/102

aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag aaa aaa att 1440  
Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile  
465 470 475 480  
aaa gag gct aag gat tgt tcc caa aaa ttt act act aag cta aaa gat 1488  
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp  
485 490 495  
agt cat gca gag ctt ggt ata caa agc gtt cag gat gat aat gca aaa 1536  
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys  
500 505 510  
aaa gct att tta aaa aca cat gga act aaa gac aag ggt gct aaa gaa 1584  
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu  
515 520 525  
ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa 1632  
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln  
530 535 540  
gca gca tta act aat tca gtt aaa gag ctt aca aat cct gtt gtg gca 1680  
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala  
545 550 555 560  
  
*A1  
Cm.1*

<210> 52  
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<212> PRT  
<213> ospC Chimera

<400> 52  
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala  
180 185 190  
Met Gly Ser Asn Ser Gly Lys Gly Asp Ser Ala Ser Thr Asn Pro  
195 200 205

99  
55/102

Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
210 215 220  
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr  
225 230 235 240  
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys  
245 250 255  
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
260 265 270  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu  
275 280 285  
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala  
290 295 300  
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala  
305 310 315 320  
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile  
325 330 335  
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
340 345 350  
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
355 360 365  
Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp  
370 375 380  
Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr  
385 390 395 400  
Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val  
405 410 415  
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala  
420 425 430  
Ile Gly Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn  
435 440 445  
Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile  
450 455 460  
Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile  
465 470 475 480  
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp  
485 490 495  
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys  
500 505 510  
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu  
515 520 525  
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln  
530 535 540  
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala  
545 550 555 560

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<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1137)

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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

100  
567102

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190

tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga 624  
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly  
195 200 205

cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt 672  
Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
210 215 220

tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa 720  
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu  
225 230 235 240

A1  
Cm.X

16  
577102

ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat 768  
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp  
245 250 255

aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata 816  
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile  
260 265 270

tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta 864  
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu  
275 280 285

aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act 912  
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr  
290 295 300

*AI*  
*un. X*

aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat 960  
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp  
305 310 315 320

gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag 1008  
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys  
325 330 335

ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca 1056  
Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser  
340 345 350

aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat 1104  
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn  
355 360 365

cct gtt gtg gca gaa agt cca aaa aaa cct taa 1137  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro \*  
370

<210> 54  
<211> 378  
<212> PRT  
<213> ospC Chimera

<400> 54  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

162  
58/102

Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190  
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly  
195 200 205  
Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
210 215 220  
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu  
225 230 235 240  
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp  
245 250 255  
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile  
260 265 270  
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu  
275 280 285  
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr  
290 295 300  
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp  
305 310 315 320  
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys  
325 330 335  
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser  
340 345 350  
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn  
355 360 365  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
370 375

<210> 55  
<211> 1158  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1) ... (1158)

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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60

163  
59/102

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
65 70 75 80  
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
Leu Leu Ala Gly Ala Tyr Ala Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
Lys Thr Asn Gly Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 576  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
180 185 190  
aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat 624  
Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn  
195 200 205  
cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa 672  
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys  
210 215 220  
att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct 720  
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala  
225 230 235 240  
ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata 768  
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile  
245 250 255  
aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg 816  
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
260 265 270  
ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt 864  
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser  
275 280 285

A1  
cm. x

164  
60/102

gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat 912  
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp  
290 295 300

tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt 960  
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu  
305 310 315 320

ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa 1008  
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys  
325 330 335

aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt 1056  
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Leu Phe  
340 345 350

aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat 1104  
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn  
355 360 365

tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa 1152  
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys  
370 375 380

cct taa 1158  
Pro \*  
385

<210> 56  
<211> 385  
<212> PRT  
<213> ospC Chimera

<400> 56  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45  
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
85 90 95  
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
100 105 110  
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
115 120 125  
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
130 135 140  
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
145 150 155 160  
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
180 185 190

A1  
cm.X

105  
61/102

Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn  
195 200 205  
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys  
210 215 220  
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala  
225 230 235 240  
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile  
245 250 255  
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
260 265 270  
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser  
275 280 285  
Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys Asp  
290 295 300  
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu  
305 310 315 320  
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys  
325 330 335  
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Leu Phe  
340 345 350  
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn  
355 360 365  
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys  
370 375 380  
Pro  
385

<210> 57  
<211> 1161  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1161)

<400> 57 48  
atg tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct  
Met Cys Ser Asn Ser Gly Lys Gly Asp Ser Ala Ser Thr Asn Pro  
1 5 10 15  
gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa 96  
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act 144  
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45  
ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa 192  
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys  
50 55 60  
ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 240  
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
65 70 75 80

16  
62/102

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu  
85 90 95

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct 336  
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala  
100 105 110

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca 384  
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala  
115 120 125

gat ctt ggc aaa cag gat gct acc gat cat gca aaa gca gct att 432  
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile  
130 135 140

tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat 480  
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
145 150 155 160

tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta 528  
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
165 170 175

act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca 576  
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro  
180 185 190

aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act 624  
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
195 200 205

aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa 672  
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
210 215 220

aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag 720  
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
225 230 235 240

gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 768  
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
245 250 255

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 816  
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
260 265 270

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 864  
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
275 280 285

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 912  
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys  
290 295 300

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 960  
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
305 310 315 320

AI  
cont

167  
63/102

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta	1008	
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu		
325	330	335
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta	1056	
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu		
340	345	350
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act	1104	
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr		
355	360	365
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa	1152	
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys		
370	375	380
aaa cct taa	1161	
Lys Pro *		
385		

A1  
cm

<210> 58  
<211> 386  
<212> PRT  
<213> ospC Chimera

<400> 58  
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro  
1 5 10 15  
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30  
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45  
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys  
50 55 60  
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
65 70 75 80  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu  
85 90 95  
Ser Lys Leu Lys Asn Leu Glu Leu Lys Thr Glu Ile Ala Lys Ala  
100 105 110  
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala  
115 120 125  
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile  
130 135 140  
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
145 150 155 160  
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
165 170 175  
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro  
180 185 190  
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
195 200 205  
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
210 215 220  
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
225 230 235 240

168  
647102

Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
245 250 255  
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
260 265 270  
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
275 280 285  
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys  
290 295 300  
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
305 310 315 320  
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
325 330 335  
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
340 345 350  
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
355 360 365  
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
370 375 380  
Lys Pro  
385

A1  
Cm<sup>c</sup>X  
<210> 59  
<211> 1197  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1197)

<400> 59 48  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110

109  
65/102

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125  
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
130 135 140  
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
145 150 155 160  
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
165 170 175  
ggt gct gaa gtt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190  
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat 672  
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
210 215 220  
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720  
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
225 230 235 240  
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc 768  
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
245 250 255  
gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct 816  
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala  
260 265 270  
aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag 864  
Lys Ala Ile Gly Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu  
275 280 285  
gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac 912  
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn  
290 295 300  
tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag 960  
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys  
305 310 315 320  
gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa 1008  
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys  
325 330 335

110  
66/102

tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056  
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp  
340 345 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104  
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly  
355 360 365

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152  
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys  
370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197  
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
385 390 395

Al X  
Cm

<210> 60  
<211> 399  
<212> PRT  
<213> ospC Chimera

<400> 60  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys 15  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60  
50 55 60  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80  
65 70 75 80  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95  
85 90 95  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110  
100 105 110  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125  
115 120 125  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140  
130 135 140  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160  
145 150 155 160  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175  
165 170 175  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 190  
180 185 190  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 205  
195 200 205  
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Ser Gly Lys Asp 220  
210 215 220  
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn 240  
225 230 235 240  
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu 255  
245 250 255  
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala 270  
260 265 270

111  
677102

Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu  
275 280 285  
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn  
290 295 300  
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys  
305 310 315 320  
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys  
325 330 335  
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp  
340 345 350  
Asn Ala Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly  
355 360 365  
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys  
370 375 380  
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
385 390 395

<210> 61  
<211> 1196  
<212> DNA  
<213> ospC Chimera

AI  
Cm +

<220>  
<221> CDS  
<222> (1)...(1196)

<400> 61 48  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80  
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95  
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110  
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125

112  
68/102

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205

cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat 672  
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
210 215 220

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720  
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
225 230 235 240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg 768  
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
245 250 255

gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct 816  
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala  
260 265 270

act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc 864  
Thr Lys Ala Ile Gly Lys Ile Gln Gln Asn Gly Gly Leu Ala Val  
275 280 285

gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca 912  
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
290 295 300

aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta 960  
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu  
305 310 315 320

aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa 1008  
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys  
325 330 335

aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat 1056  
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp  
340 345 350

AI  
cm.t

gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag 1104  
 Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys  
 355 360 365  
 ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca 1152  
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala  
 370 375 380  
 aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac 1196  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
 385 390 395

<210> 62  
 <211> 398  
 <212> PRT  
 <213> ospC Chimera

<400> 62  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
 210 215 220  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 225 230 235 240  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
 245 250 255  
 Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala  
 260 265 270  
 Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val  
 275 280 285  
 Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 290 295 300

A1  
 Con't

114  
707102

Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu  
305 310 315 320  
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys  
325 330 335  
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp  
340 345 350  
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys  
355 360 365  
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala  
370 375 380  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
385 390 395  
385

<210> 63  
<211> 1185  
<212> DNA  
<213> ospC Chimera

A1  
Cont.

<220>  
<221> CDS  
<222> (1)...(1185)

<400> 63 48  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Tyr Thr Ile Ser  
100 105 110  
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140

115  
717102

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528  
Glu Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205

agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct 672  
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
210 215 220

AI  
cont

gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720  
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa 768  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255

gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt 816  
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly  
260 265 270

aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac 864  
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn  
275 280 285

gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa 912  
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys  
290 295 300

aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa 960  
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu  
305 310 315 320

aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa 1008  
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu  
325 330 335

cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa 1056  
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asn Ala Lys Lys  
340 345 350

gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt 1104  
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu  
355 360 365

116  
27102

gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag 1152  
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu  
370 375 380

atg ctt act aat tca gtt aaa gag ctt aca agc 1185  
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
385 390 395

**AI**  
**Cr.**  
<210> 64  
<211> 395  
<212> PRT  
<213> ospC Chimera

<400> 64  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205  
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
210 215 220  
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
225 230 235 240  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255  
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly  
260 265 270  
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn  
275 280 285  
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys  
290 295 300  
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu  
305 310 315 320  
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu  
325 330 335  
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys  
340 345 350

117  
73/102

Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu  
355 360 365  
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu  
370 375 380  
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
385 390 395

<210> 65  
<211> 1184  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1184)

A1  
Cn  
<400> 65 48  
atg aga tta tta ata gga ttt gct tta gct tta ata gga tgt  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
Ala Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160

118  
747102

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190  
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205  
agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct 672  
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
210 215 220  
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720  
Al Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
Cm 225 230 235 240  
agt aaa aaa att aca gaa tct aac gca gtt ctg gct gtg aaa gaa 768  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255  
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att 816  
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
260 265 270  
gtt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat 864  
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His  
275 280 285  
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca 912  
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr  
290 295 300  
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att 960  
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Ile  
305 310 315 320  
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga 1008  
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly  
325 330 335  
gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa 1056  
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys  
340 345 350  
aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag 1104  
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu  
355 360 365  
ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa 1152  
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Lys  
370 375 380  
gag atg ctt gct aat tca gtt aaa gag ctt ac 1184  
Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
385 390

19  
75/102

<210> 66  
<211> 394  
<212> PRT  
<213> ospC Chimera

<400> 66  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
Lys Gly Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205  
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
210 215 220  
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
225 230 235 240  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255  
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
260 265 270  
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His  
275 280 285  
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr  
290 295 300  
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile  
305 310 315 320  
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly  
325 330 335  
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys  
340 345 350  
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu  
355 360 365  
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys  
370 375 380  
Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
385 390

AI  
cm.t

120  
76/102

<210> 67  
<211> 1184  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1184)

**AI**  
**Cm.t**

<400> 67  
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
Leu Ala Val Lys Glu Val Ala Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160  
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190

121  
~~777102~~

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205

agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct 672  
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser  
210 215 220

aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720  
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa 768  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255

gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att 816  
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
260 265 270

ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac 864  
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn  
275 280 285

aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa 912  
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu  
290 295 300

aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca 960  
Lys Leu Asn Val Leu Lys Asn Glu Leu Lys Glu Lys Ile Asp Thr  
305 310 315 320

gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat 1008  
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His  
325 330 335

gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct 1056  
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala  
340 345 350

att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa 1104  
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu  
355 360 365

aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca 1152  
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr  
370 375 380

tta aaa aat gct gtt aaa gag ctt aca agt cc 1184  
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser  
385 390

<210> 68  
<211> 394  
<212> PRT  
<213> ospC Chimera

<400> 68

122  
78/102

Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
Lys Gly Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205  
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser  
210 215 220  
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
225 230 235 240  
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
245 250 255  
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
260 265 270  
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn  
275 280 285  
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu  
290 295 300  
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr  
305 310 315 320  
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His  
325 330 335  
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala  
340 345 350  
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu  
355 360 365  
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr  
370 375 380  
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser  
385 390

<210> 69  
<211> 1209  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS

123  
79102

<222> (1) ... (1209)

**A1**  
**cmx**

<400> 69  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
Ala Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160  
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190  
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205  
agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act 672  
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
210 215 220

124  
80/102

aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa 720  
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
225 230 235 240  
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag 768  
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
245 250 255  
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 816  
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
260 265 270  
ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 864  
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
275 280 285  
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 912  
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
290 295 300  
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 960  
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys  
305 310 315 320  
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 1008  
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
325 330 335  
ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1056  
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
340 345 350  
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1104  
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
355 360 365  
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1152  
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
370 375 380  
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1200  
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
385 390 395 400  
aaa cct taa 1209  
Lys Pro \*

<210> 70  
<211> 402  
<212> PRT  
<213> ospC Chimera

<400> 70  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

A1  
cm. x

125

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Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175  
Lys Gly Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205  
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
210 215 220  
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
225 230 235 240  
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
245 250 255  
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
260 265 270  
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
275 280 285  
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
290 295 300  
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys  
305 310 315 320  
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
325 330 335  
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
340 345 350  
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
355 360 365  
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
370 375 380  
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
385 390 395 400  
Lys Pro

<210> 71  
<211> 1179  
<212> DNA  
<213> ospC Chimera  
  
<220>  
<221> CDS  
<222> (1)...(1179)

126  
82/102

<400> 71  
 atg aga tta tta ata gga ttt gct tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60  
 ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 65 70 75 80  
 gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288  
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
 85 90 95  
 aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
 100 105 110  
 gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
 115 120 125  
 gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
 130 135 140  
 cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
 145 150 155 160  
 aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528  
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
 165 170 175  
 gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576  
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
 180 185 190  
 gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
 195 200 205  
 att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat 672  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
 210 215 220

127  
83/102

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa 768  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
245 250 255

act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa 816  
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys  
260 265 270

ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca 864  
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser  
275 280 285

tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata 912  
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile  
290 295 300

agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct 960  
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala  
305 310 315 320

aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca 1008  
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr  
325 330 335

gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att 1056  
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile  
340 345 350

tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag 1104  
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys  
355 360 365

tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt 1152  
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu  
370 375 380

act aat tca gtt aaa gag ctt aca agc 1179  
Thr Asn Ser Val Lys Glu Leu Thr Ser  
385 390

<210> 72  
<211> 393  
<212> PRT  
<213> ospC Chimera

<400> 72  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
50 55 60

AI  
Cr

128  
84/102

Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
85 90 95  
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
100 105 110  
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160  
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
165 170 175  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180 185 190  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195 200 205  
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
210 215 220  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225 230 235 240  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
245 250 255  
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys  
260 265 270  
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser  
275 280 285  
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile  
290 295 300  
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala  
305 310 315 320  
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr  
325 330 335  
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile  
340 345 350  
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys  
355 360 365  
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu  
370 375 380  
Thr Asn Ser Val Lys Glu Leu Thr Ser  
385 390

<210> 73  
<211> 1178  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1178)

<400> 73  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

129  
85/102

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
50 55 60

ctg gcc, gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240  
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288  
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336  
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384  
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528  
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195 200 205

att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat 672  
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
210 215 220

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa 768  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu  
245 250 255

A' cm X

act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa 816  
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
 260 265 270  
 aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga 864  
 Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly  
 275 280 285  
 aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa 912  
 Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys  
 290 295 300  
 tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat 960  
 Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn  
 305 310 315 320  
 gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat 1008  
 Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His  
 325 330 335  
 gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct 1056  
 Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala  
 340 345 350  
 att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa 1104  
 Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu  
 355 360 365  
 aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg 1152  
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met  
 370 375 380  
 ctt gct aat tca gtt aaa gag ctt ac 1178  
 Leu Ala Asn Ser Val Lys Glu Leu  
 385 390

A1  
 cm.x

<210> 74  
 <211> 392  
 <212> PRT  
 <213> ospC Chimera

<400> 74  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 65 70 75 80  
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
 85 90 95  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
 100 105 110

131  
-874102

Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160  
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
165 170 175  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180 185 190  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195 200 205  
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
210 215 220  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225 230 235 240  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu  
245 250 255  
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
260 265 270  
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly  
275 280 285  
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys  
290 295 300  
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn  
305 310 315 320  
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His  
325 330 335  
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala  
340 345 350  
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu  
355 360 365  
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met  
370 375 380  
Leu Ala Asn Ser Val Lys Glu Leu  
385 390

A1  
cont  
<210> 75  
<211> 1178  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1178)

<400> 75 48  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

132  
-007102

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240  
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288  
Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala  
85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336  
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384  
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125

gaa aag att gat aca gct aag caa tgt tot aca gaa ttt act aat aaa 432  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528  
Asn Ala Gln Arg Ala Ile Leu Lys His Ala Asn Lys Asp Lys Gly  
165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195 200 205

att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat 672  
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn  
210 215 220

tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag 768  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
245 250 255

acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag 816  
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
260 265 270

Al  
cm +

133  
897102

aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca 864  
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser  
275 280 285

ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta 912  
Leu Leu Ser Gly Ala Tyr Ala Ser Asp Leu Ile Ala Glu Lys Leu  
290 295 300

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag 960  
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys  
305 310 315 320

caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg 1008  
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val  
325 330 335

ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta 1056  
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu  
340 345 350

aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta 1104  
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu  
355 360 365

ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa 1152  
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys  
370 375 380

aat gct gtt aaa gag ctt aca agt cc 1178  
Asn Ala Val Lys Glu Leu Thr Ser  
385 390

<210> 76  
<211> 392  
<212> PRT  
<213> ospC Chimera

<400> 76  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
50 55 60  
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
65 70 75 80  
Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala  
85 90 95  
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
100 105 110  
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
115 120 125  
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
130 135 140  
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
145 150 155 160

A1  
cm.†

134  
90/102

AI  
Cm.f

Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
165 170 175  
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
180 185 190  
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
195 200 205  
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn  
210 215 220  
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
225 230 235 240  
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
245 250 255  
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
260 265 270  
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser  
275 280 285  
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu  
290 295 300  
Asn Val Leu Lys Asn Glu Leu Lys Glu Ile Asp Thr Ala Lys  
305 310 315 320  
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val  
325 330 335  
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu  
340 345 350  
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Lys Leu  
355 360 365  
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys  
370 375 380  
Asn Ala Val Lys Glu Leu Thr Ser  
385

<210> 77  
<211> 1230  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1230)

<400> 77  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt  
15  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
5  
1

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa  
20  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Ser Gly Lys  
25  
30

gat ggg aat aca tct gca aat tct gct gat gag tct aat ggg cct  
35  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
40  
45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta  
50  
Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
55  
60  
192

135  
91/102

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80  
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95  
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110  
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125  
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Ser Glu Thr Phe Thr Asn  
130 135 140  
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
145 150 155 160  
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
165 170 175  
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190  
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca 672  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser  
210 215 220  
ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct 720  
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro  
225 230 235 240  
aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta 768  
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu  
245 250 255  
ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt 816  
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu  
260 265 270  
tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac 864  
Ser Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn  
275 280 285  
gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca 912  
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser  
290 295 300

AI  
CR

136  
~~99/102~~

aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag	960		
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys			
305	310	315	320
aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag	1008		
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys			
325	330	335	
ct aaaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat	1056		
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp			
340	345	350	
aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt	1104		
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly			
355	360	365	
gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa	1152		
Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys			
370	375	380	
gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct	1200		
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro			
385	390	395	400
gtt gtg gca gaa agt cca aaa aaa cct taa	1230		
Val Val Ala Glu Ser Pro Lys Lys Pro *			
405			

<210> 78  
<211> 409  
<212> PRT  
<213> ospC Chimera

<400> 78  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175

137  
93/102

*AI X*  
*CM*

Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser  
210 215 220  
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro  
225 230 235 240  
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu  
245 250 255  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
260 265 270  
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn  
275 280 285  
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser  
290 295 300  
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys  
305 310 315 320  
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys  
325 330 335  
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp  
340 345 350  
Asn Ala Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly  
355 360 365  
Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys  
370 375 380  
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro  
385 390 395 400  
Val Val Ala Glu Ser Pro Lys Lys Pro  
405

<210> 79  
<211> 1209  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1209)

<400> 79 48  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60

138  
947102

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80  
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95  
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110  
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125  
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
130 135 140  
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
145 150 155 160  
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
165 170 175  
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190  
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser  
210 215 220  
ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720  
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
225 230 235 240  
ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca 768  
Gly Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala  
245 250 255  
gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat 816  
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp  
260 265 270  
gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta 864  
Glu Leu Ala Lys Ala Ile Gly Lys Ile Lys Asn Asp Val Ser Leu  
275 280 285  
gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta 912  
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu  
290 295 300

A  
Cm. t

139  
95/102

att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga 960  
att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga  
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly 320  
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly  
315 310  
305 305  
gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt 1008  
gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt  
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe 335  
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe  
325 330  
act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt 1056  
act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt  
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val 350  
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val  
345 340  
act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa 1104  
act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa  
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys 365  
355 360  
act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac 1152  
act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac  
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn 380  
375 370  
ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt 1200  
ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt  
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu 400  
385 390  
1209  
aca agc taa  
Thr Ser \*

A1  
Cm<sup>x</sup>  
<210> 80  
<211> 402  
<212> PRT  
<213> ospC Chimera

<400> 80  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys 15  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys 15  
5 10  
1 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30  
20 25  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45  
35 40  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60  
50 55  
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Ile 80  
65 70 75  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95  
85 90  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110  
100 105  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125  
115 120  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140  
130 135  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160  
145 150 155  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175  
165 170

140  
26/102

Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser  
210 215 220  
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
225 230 235 240  
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala  
245 250 255  
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp  
260 265 270  
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu  
275 280 285  
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu  
290 295 300  
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly  
305 310 315 320  
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe  
325 330 335  
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val  
340 345 350  
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys  
355 360 365  
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn  
370 375 380  
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu  
385 390 395 400  
Thr Ser

A1  
Cm.  
<210> 81  
<211> 1205  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1205)

<400> 81 48  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys 15  
1 5 10  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
gat ggg aat aca tct gca aat tct gct gat gag tct aat ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60

141  
97/102

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
 Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 100 105 110  
 aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser  
 210 215 220  
 gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720  
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
 225 230 235 240  
 ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca 768  
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala  
 245 250 255  
 gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat 816  
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp  
 260 265 270  
 gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt 864  
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly  
 275 280 285  
 tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat 912  
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr  
 290 295 300

A1  
Cf

142  
98/102

960  
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca  
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca  
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser  
305 310 315 320  
gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat 1008  
gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat  
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp  
325 330 335  
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat 1056  
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat  
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn  
340 345 350  
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct 1104  
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct  
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala  
355 360 365  
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa 1152  
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa  
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu  
370 375 380  
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag 1200  
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag  
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu  
385 390 395  
ctt ac 1205  
Leu

A)  
Cm. +  
<210> 82  
<211> 401  
<212> PRT  
<213> ospC Chimera

<400> 82  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
130 135 140  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
145 150 155 160  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
165 170 175  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser

143  
99/102

180 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
185 200 205  
195 Pro Val Val Ala Glu Ser Pro Ser Met Val Asn Asn Ser  
210 215 220  
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
225 230 235 240  
Gly Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala  
245 250 255  
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp  
260 265 270  
Glu Leu Ala Thr Lys Ala Ile Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr  
275 280 285  
Leu Ala Val Glu Ala Gly His Asn Gly Leu Lys Asn Ser  
290 295 300 320  
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser  
305 310 315 330 335  
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp  
325 340 345 350  
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn  
355 360 365 380 400  
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala  
370 375 390 395  
Lys Asp Lys Gly Ala Ala Glu Leu Lys Leu Phe Lys Ala Val Glu  
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu  
385  
Leu

AI  
cont'd  
<210> 83  
<211> 1236  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
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<400> 83  
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
gca caa aaa ggt gct gag tca att gga tcc tgt agt aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys  
20 25 30

ggt ggg gat tct gca tct act aat cct gct gag tct gcg aaa ggg 144  
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly  
35 40 45

cct aat ctt aca gaa ata agc aaa att aca gat tct aat gca ttt 192  
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
50 55 60

A1  
cont

144  
100/102

gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa 240  
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Ser Ile Asp Glu  
70 75 80

65 ctt gct aag aaa gct att ggt caa aaa ata gac aat aat ggt tta 288  
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Gly Leu  
85 90 95

gct gct tta aat aat cag aat gga tcg ttg tta gca gga gcc tat gca 336  
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala  
100 105 110

ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aat tta gaa 384  
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu  
115 120 125

gaa tta aag aca gaa att gca aag gct aag aaa ttg tcc gaa gaa ttt 432  
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Cys Ser Glu Glu Phe  
130 135 140

act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct 480  
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala  
145 150 155 160

acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc 528  
Thr Asp Asp His Ala Lys Ala Ile Leu Lys Thr His Ala Thr Thr  
165 170 175

gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt 576  
Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly  
180 185 190

ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt 624  
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu  
195 200 205

aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat 672  
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn  
210 215 220

aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa 720  
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys  
225 230 235 240

gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca 768  
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala  
245 250 255

ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat 816  
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp  
260 265 270

gaa ctt tct aaa gct att ggt aaa aaa aat gat ggt act tta 864  
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu  
275 280 285

gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa 912  
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu  
290 295 300

145  
101/102

ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa 960  
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu  
305 310 315 320  
tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act 1008  
Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr  
325 330 335  
act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag 1056  
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln  
340 345 350  
gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac 1104  
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp  
355 360 365  
aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg 1152  
Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu  
370 375 380  
tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca 1200  
Ser Lys Ala Ala Gln Ala Leu Thr Asn Ser Val Lys Glu Leu Thr  
385 390 395 400  
aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 1236  
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro \*  
405

*Al*  
*cm*

<210> 84  
<211> 411  
<212> PRT  
<213> ospC Chimera

<400> 84  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys  
20 25 30  
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly  
35 40 45  
Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Phe  
50 55 60 65  
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu  
65 70 75 80  
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu  
85 90 95  
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala  
100 105 110  
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu  
115 120 125  
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe  
130 135 140  
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala  
145 150 155 160  
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr  
165 170 175

146  
~~102-102~~

Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly  
180 185 190  
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu  
195 200 205  
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn  
210 215 220  
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys  
225 230 235 240  
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala  
245 250 255  
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp  
260 265 270  
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu  
275 280 285  
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu  
290 295 300  
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu  
305 310 315 320  
Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr  
325 330 335  
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln  
340 345 350  
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp  
355 360 365  
Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu  
370 375 380  
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr  
385 390 395 400  
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
405 410

*AI concd.*